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#4

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/991,211

DATE: 04/24/2002

TIME: 10:16:06

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Output Set: N:\CRF3\04242002\I991211.raw

ENTERED

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1 <110> APPLICANT: Pharmacia & Upjohn
2 <120> TITLE OF INVENTION: CRYSTALLIZATION AND STRUCTURE DETERMINATION OF
3   STAPHYLOCOCCUS AUREUS
4   UDP-N-ACETYLENOLPYRUVYLGLUCOSAMINE REDUCTASE (S. aureus
5   MurB)
6 <130> FILE REFERENCE: 268.6241 0101
7 <140> CURRENT APPLICATION NUMBER: 09/991,211
8 <141> CURRENT FILING DATE: 2001-11-21
10 <150> PRIOR APPLICATION NUMBER: 09/632,947
11 <151> PRIOR FILING DATE: 2000-08-04
14 <150> PRIOR APPLICATION NUMBER: 60/147,164
15 <151> PRIOR FILING DATE: 1999-08-04
16 <160> NUMBER OF SEQ ID NOS: 11
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 326
21 <212> TYPE: PRT
22 <213> ORGANISM: Staphylococcus aureus
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24   Met Arg Gly Ser His His His His His His Thr Asp Pro Ile Asn Lys
25       1               5               10               15
26   Asp Ile Tyr Gln Ala Leu Gln Gln Leu Ile Pro Asn Glu Lys Ile Lys
27       20               25               30
28   Val Asp Glu Pro Leu Lys Arg Tyr Thr Tyr Thr Lys Thr Gly Gly Asn
29       35               40               45
30   Ala Asp Phe Tyr Ile Thr Pro Thr Lys Asn Glu Glu Val Gln Ala Val
31       50               55               60
32   Val Lys Tyr Ala Tyr Gln Asn Glu Ile Pro Val Thr Tyr Leu Gly Asn
33       65               70               75               80
34   Gly Ser Asn Ile Ile Ile Arg Glu Gly Gly Ile Arg Gly Ile Val Ile
35       85               90               95
36   Ser Leu Leu Ser Leu Asp His Ile Glu Val Ser Asp Asp Ala Ile Ile
37       100              105              110
38   Ala Gly Ser Gly Ala Ala Ile Ile Asp Val Ser Arg Val Ala Arg Asp
39       115              120              125
40   Tyr Ala Leu Thr Gly Leu Glu Phe Ala Cys Gly Ile Pro Gly Ser Ile
41       130              135              140
42   Gly Gly Ala Val Tyr Met Asn Ala Gly Ala Tyr Gly Gly Glu Val Lys
43       145              150              155              160
44   Asp Cys Ile Asp Tyr Ala Leu Cys Val Asn Glu Gln Gly Ser Leu Ile
45       165              170              175
46   Lys Leu Thr Thr Lys Glu Leu Glu Leu Asp Tyr Arg Asn Ser Ile Ile
47       180              185              190

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48      Gln Lys Glu His Leu Val Val Leu Glu Ala Ala Phe Thr Leu Ala Pro
49              195                      200                      205
50      Gly Lys Met Thr Glu Ile Gln Ala Lys Met Asp Asp Leu Thr Glu Arg
51              210                      215                      220
52      Arg Glu Ser Lys Gln Pro Leu Glu Tyr Pro Ser Cys Gly Ser Val Phe
53      225                      230                      235                      240
54      Gln Arg Pro Pro Gly His Phe Ala Gly Lys Leu Ile Gln Asp Ser Asn
55              245                      250                      255
56      Leu Gln Gly His Arg Ile Gly Gly Val Glu Val Ser Thr Lys His Ala
57              260                      265                      270
58      Gly Phe Met Val Asn Val Asp Asn Gly Thr Ala Thr Asp Tyr Glu Asn
59              275                      280                      285
60      Leu Ile His Tyr Val Gln Lys Thr Val Lys Glu Lys Phe Gly Ile Glu
61              290                      295                      300
62      Leu Asn Arg Glu Val Arg Ile Ile Gly Glu His Pro Lys Glu Ser Leu
63      305                      310                      315                      320
64      Gln Pro Ser Leu Ile Ser
65              325
67 <210> SEQ ID NO: 2
68 <211> LENGTH: 342
69 <212> TYPE: PRT
70 <213> ORGANISM: Escherichia coli
71 <400> SEQUENCE: 2
72      Met Asp His Ser Leu Lys Pro Trp Asn Thr Phe Gly Ile Asp His Asn
73              1                      5                      10                      15
74      Ala Gln His Ile Val Cys Ala Glu Asp Glu Gln Gln Leu Leu Asn Ala
75              20                      25                      30
76      Trp Gln Tyr Ala Thr Ala Glu Gly Gln Pro Val Leu Ile Leu Gly Glu
77              35                      40                      45
78      Gly Ser Asn Val Leu Phe Leu Glu Asp Tyr Arg Gly Thr Val Ile Ile
79              50                      55                      60
80      Asn Arg Ile Lys Gly Ile Glu Ile His Asp Glu Pro Asp Ala Trp Tyr
81      65                      70                      75                      80
82      Leu His Val Gly Ala Gly Glu Asn Trp His Arg Leu Val Lys Tyr Thr
83              85                      90                      95
84      Leu Gln Glu Gly Met Pro Gly Leu Glu Asn Leu Ala Leu Ile Pro Gly
85              100                      105                      110
86      Cys Val Gly Ser Ser Pro Ile Gln Asn Ile Gly Ala Tyr Gly Val Glu
87              115                      120                      125
88      Leu Gln Arg Val Cys Ala Tyr Val Asp Ser Val Glu Leu Ala Thr Gly
89              130                      135                      140
90      Lys Gln Val Arg Leu Thr Ala Lys Glu Cys Arg Phe Gly Tyr Arg Asp
91      145                      150                      155                      160
92      Ser Ile Phe Lys His Glu Tyr Gln Asp Arg Phe Ala Ile Val Ala Val
93              165                      170                      175
94      Gly Leu Arg Leu Pro Lys Glu Trp Gln Pro Val Leu Thr Tyr Gly Asp
95              180                      185                      190
96      Leu Thr Arg Leu Asp Pro Thr Thr Val Thr Pro Gln Gln Val Phe Asn
97              195                      200                      205

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98      Ala Val Cys His Met Arg Thr Thr Lys Leu Pro Asp Pro Lys Val Asn
99          210                      215                      220
100     Gly Asn Ala Gly Ser Phe Phe Lys Asn Pro Val Val Ser Ala Glu Thr
101     225                      230                      235                      240
102     Ala Lys Ala Leu Leu Ser Gln Phe Pro Thr Ala Pro Asn Tyr Pro Gln
103     245                      250                      255
104     Ala Asp Gly Ser Val Lys Leu Ala Ala Gly Trp Leu Ile Asp Gln Cys
105     260                      265                      270
106     Gln Leu Lys Gly Met Gln Ile Gly Gly Ala Ala Val His Arg Gln Gln
107     275                      280                      285
108     Ala Leu Val Leu Ile Asn Glu Asp Asn Ala Lys Ser Glu Asp Val Val
109     290                      295                      300
110     Gln Leu Ala His His Val Arg Gln Lys Val Gly Glu Lys Phe Asn Val
111     305                      310                      315                      320
112     Trp Leu Glu Pro Glu Val Arg Phe Ile Gly Ala Ser Gly Glu Val Ser
113     325                      330                      335
114     Ala Val Glu Thr Ile Ser
115     340
117 <210> SEQ ID NO: 3
118 <211> LENGTH: 259
119 <212> TYPE: PRT
120 <213> ORGANISM: Helicobacter pylori
121 <400> SEQUENCE: 3
122     Met Leu Glu Thr Thr Ile Asp Phe Ser Arg Tyr Ser Ser Val Lys Ile
123     1                      5                      10                      15
124     Gly Thr Pro Leu Lys Val Ser Val Leu Glu Asn Asp Asp Glu Ile Ser
125     20                      25                      30
126     Gln Glu His Gln Ile Ile Gly Leu Ala Asn Asn Leu Leu Ile Ala Pro
127     35                      40                      45
128     Ser Ala Lys Asn Leu Ala Leu Leu Gly Lys Asn Tyr Asp Tyr Ile Cys
129     50                      55                      60
130     Asp Lys Gly Glu Cys Val Glu Ile Gly Gly Ala Ala Asn Ala Ser Lys
131     65                      70                      75                      80
132     Ile Phe Asn Tyr Phe Arg Ala Asn Asp Leu Glu Gly Leu Glu Phe Leu
133     85                      90                      95
134     Gly Gln Leu Pro Gly Thr Leu Gly Ala Leu Val Lys Met Asn Ala Gly
135     100                     105                     110
136     Met Lys Glu Phe Glu Ile Lys Asn Val Leu Glu Ser Ala Cys Ile Asn
137     115                     120                     125
138     Asn Gln Trp Leu Glu Lys Glu Ala Leu Gly Leu Gly Tyr Arg Ser Ser
139     130                     135                     140
140     Gly Phe Ser Gly Val Val Leu Arg Ala Arg Phe Lys Lys Thr His Gly
141     145                     150                     155                     160
142     Phe Arg Glu Gly Val Leu Lys Ala Cys Gln Ser Met Arg Lys Ser His
143     165                     170                     175
144     Pro Lys Leu Pro Asn Phe Gly Ser Cys Phe Lys Asn Pro Pro Asn Asp
145     180                     185                     190
146     His Ala Gly Arg Leu Leu Glu Gly Val Gly Leu Arg Gly Tyr Cys Leu
147     195                     200                     205

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148   Lys Arg Val Gly Phe Ala Lys Glu His Ala Asn Phe Leu Val Asn Leu
149           210                215                220
150   Gly Gly Ala Glu Phe Glu Glu Ala Leu Asp Leu Ile Glu Leu Ala Lys
151       225                230                235                240
152   Ala Arg Val Leu Gln Glu Tyr Gly Ile His Leu Glu Glu Glu Val Lys
153           245                250                255
154   Ile Leu Arg
156 <210> SEQ ID NO: 4
157 <211> LENGTH: 297
158 <212> TYPE: PRT
159 <213> ORGANISM: Aquifex aeolicus
160 <400> SEQUENCE: 4
161   Met Leu Phe Leu Lys Asn Val Pro Leu Gln Asn Leu Thr Thr Ile Lys
162       1                5                10                15
163   Ile Gly Gly Arg Val Ser Phe Tyr Ala Glu Pro Ser Asp Leu Lys Glu
164           20                25                30
165   Ile Ser Leu Cys Ile Asp Phe Ser Lys Ser Arg Asp Ile Pro Leu Phe
166       35                40                45
167   Val Leu Gly Asn Gly Ser Asn Thr Ile Phe Gly Asp Val Arg Gly Leu
168       50                55                60
169   Val Val Asn Leu Lys Asn Leu Lys Gly Phe Lys Val Lys Glu Ile Lys
170       65                70                75                80
171   Gly Lys Phe Phe Val Glu Ala Phe Ser Gly Thr Pro Leu Lys Asp Leu
172           85                90                95
173   Ile Arg Phe Ser Val Lys Glu Asn Val Lys Ser Phe Tyr Lys Leu Leu
174           100               105               110
175   Gly Phe Pro Ala Ser Val Gly Gly Ala Val Ser Met Asn Ala Gly Ala
176       115               120               125
177   Phe Gly Val Glu Ile Ser Asp Phe Leu Lys Glu Val Tyr Phe Val Asp
178       130               135               140
179   Trp Glu Gly Lys Leu Gln Lys Ala Lys Arg Asp Glu Leu Asn Phe Ser
180       145               150               155               160
181   Tyr Arg Lys Ser Pro Phe Pro Lys Leu Gly Ile Val Phe Lys Val Val
182           165               170               175
183   Phe Glu Phe Glu Arg Ser Lys Glu Asn Ile Leu Pro Lys Tyr Glu Lys
184       180               185               190
185   Ile Arg Arg Ile Arg Lys Glu Lys Gln Pro Ile Asn Leu Pro Thr Ser
186       195               200               205
187   Gly Ser Thr Phe Lys Asn Pro Glu Gly Asn Phe Ala Gly Lys Leu Leu
188       210               215               220
189   Glu Lys Ala Gly Leu Lys Gly Phe Arg Leu Lys Asn Val Gly Phe Ser
190       225               230               235               240
191   Glu Lys His Ala Asn Phe Leu Val Asn Tyr Gly Gly Gly Thr Phe Ser
192           245               250               255
193   Glu Val Val Asp Leu Ile Asn Ile Ala Lys Glu Arg Val Tyr Glu Asn
194           260               265               270
195   Phe Gly Ile Val Leu Glu Glu Glu Val Lys Leu Ile Glu Ser Ser Gly
196       275               280               285
197   Ser Asp Gly Trp Lys Val Leu Gly Ala

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198          290          295
200 <210> SEQ ID NO: 5
201 <211> LENGTH: 303
202 <212> TYPE: PRT
203 <213> ORGANISM: Bacillus subtilis
204 <400> SEQUENCE: 5
205 Met Glu Lys Val Ile Gln Glu Leu Lys Glu Arg Glu Val Gly Lys Val
206      1              5              10              15
207 Leu Ala Asn Glu Pro Leu Ala Asn His Thr Thr Met Lys Ile Gly Gly
208      20              25              30
209 Pro Ala Asp Val Leu Val Ile Pro Ser Ser Val Asp Ala Val Lys Asp
210      35              40              45
211 Ile Met Asp Val Ile Lys Lys Tyr Asp Val Lys Trp Thr Val Ile Gly
212      50              55              60
213 Arg Gly Ser Asn Leu Leu Val Leu Asp Glu Gly Ile Arg Gly Val Val
214      65              70              75              80
215 Ile Lys Leu Gly Ala Gly Leu Asp His Leu Glu Leu Glu Gly Glu Gln
216      85              90              95
217 Val Thr Val Gly Gly Gly Tyr Ser Val Val Arg Leu Ala Thr Ser Leu
218      100             105             110
219 Ser Lys Lys Gly Leu Ser Gly Leu Glu Phe Ala Ala Gly Ile Pro Gly
220      115             120             125
221 Ser Val Gly Gly Ala Val Tyr Met Asn Ala Gly Ala His Gly Ser Asp
222      130             135             140
223 Met Ser Glu Ile Leu Val Lys Ala His Ile Leu Phe Glu Asp Gly Thr
224      145             150             155             160
225 Ile Glu Trp Leu Thr Asn Glu Gln Met Asp Phe Ser Tyr Arg Thr Ser
226      165             170             175
227 Val Leu Gln Lys Lys Arg Pro Gly Val Cys Leu Glu Ala Val Leu Gln
228      180             185             190
229 Leu Glu Gln Lys Asp Lys Glu Ser Ile Val Gln Gln Met Gln Ser Asn
230      195             200             205
231 Lys Asp Tyr Arg Lys Asn Thr Gln Pro Tyr Ser Ser Pro Cys Ala Gly
232      210             215             220
233 Ser Ile Phe Arg Asn Pro Leu Pro Asn His Ala Gly Asn Leu Val Glu
234      225             230             235             240
235 Lys Ala Gly Leu Lys Gly Tyr Gln Ile Gly Gly Ala Lys Ile Ser Glu
236      245             250             255
237 Met His Gly Asn Phe Ile Val Asn Ala Gly Gly Ala Ser Ala Lys Asp
238      260             265             270
239 Val Leu Asp Leu Ile Asp His Val Lys Lys Thr Ile Arg Glu Lys Tyr
240      275             280             285
241 Glu Ile Asp Met His Thr Glu Val Glu Ile Ile Gly Gly Asn Arg
242      290             295             300
244 <210> SEQ ID NO: 6
245 <211> LENGTH: 302
246 <212> TYPE: PRT
247 <213> ORGANISM: Borrelia burgdorferi
248 <400> SEQUENCE: 6

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VERIFICATION SUMMARY

DATE: 04/24/2002

PATENT APPLICATION: US/09/991,211

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